

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/760,723

DATE: 06/08/2001

TIME: 17:04:59

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Output Set: N:\CRF3\06082001\I760723.raw

3 <110> APPLICANT: KOISHIHARA, YASUO
 5 <120> TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
 7 <130> FILE REFERENCE: 053466/0295
 9 <140> CURRENT APPLICATION NUMBER: 09/760,723
 C--> 10 <141> CURRENT FILING DATE: 2001-05-29
 12 <150> PRIOR APPLICATION NUMBER: 09/367,833
 13 <151> PRIOR FILING DATE: 1998-08-25
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00831
 16 <151> PRIOR FILING DATE: 1998-02-27
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1016
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (23)..(562)
 30 <223> OTHER INFORMATION: Nucleotide sequence of DNA coding for Hm1.24
 31 antigen
 33 <400> SEQUENCE: 1
 34 gaattcggca cgagggatct gg atg gca tct act tcg tat gac tat tgc aga 52
 35 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg
 36 1 5 10
 38 gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg ata 100
 39 Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile
 40 15 20 25
 42 gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg att 148
 43 Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu Ile
 44 30 35 40
 46 atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt cgg 196
 47 Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg
 48 45 50 55
 50 gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag ctg 244
 51 Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu
 52 60 65 70
 54 acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc acc 292
 55 Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr
 56 75 80 85 90
 58 tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag aag 340
 59 Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys
 60 95 100 105
 62 gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act aca 388
 63 Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr
 64 110 115 120
 66 tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg aga 436
 67 Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg

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68          125          130          135
70 aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac tac 484
71 Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr
72          140          145          150
74 ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg att 532
75 Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile
76 155          160          165          170
78 gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 582
79 Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
80          175          180
82 acatcttggg aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 642
84 ttctgagcgg gtcattgggg aacacgggta gcggggagag cacggggtag ccggagaagg 702
86 gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 762
88 ttgaccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgct 822
90 tcccaccctg agattgggca tgggggtgcg tgtggggggc atgtgctgcc tgttggtatg 882
92 gggttttttt gcgggggggg ttgctttttt ctgggggtct tgagctccaa aaaaataaac 942
94 acttcctttg agggagagca ccacacctta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1002
96 ttcgggcggc cgcc 1016
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101 <211> LENGTH: 379
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA encoding L
107 chain V region version of a humanized anti-HM1.24
108 antibody
110 <220> FEATURE:
111 <221> NAME/KEY: CDS
112 <222> LOCATION: (1)..(378)
114 <220> FEATURE:
115 <221> NAME/KEY: sig_peptide/
116 <222> LOCATION: (1)..(57)
118 <220> FEATURE:
119 <221> NAME/KEY: mat_peptide
120 <222> LOCATION: (58)..(378)
122 <400> SEQUENCE: 2
123 atg gga tgg agc tgt atc atc ctc tcc ttg gta gca aca gct aca ggt 48
124 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
125          -15          -10          -5
127 gtc cac tcc gac atc cag atg acc cag agc cca agc agc ctg agc gcc 96
128 Val His Ser Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
129          -1 1          5          10
131 agc gtg ggt gac aga gtg acc atc acc tgt aag gct agt cag gat gtg 144
132 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
133          15          20          25
135 aat act gct gta gcc tgg tac cag cag aag cca gga aag gct cca aag 192
136 Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
137 30          35          40          45
139 ctg ctg atc tac tcg gca tcc aac cgg tac act ggt gtg cca agc aga 240

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140 Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
141          50          55          60
143 ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc 288
144 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
145          65          70          75
147 ctc cag cca gag gac atc gct acc tac tac tgc cag caa cat tat agt 336
148 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser
149          80          85          90
151 act cca ttc acg ttc ggc caa ggg acc aag gtg gaa atc aaac 379
152 Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
153          95          100          105
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 418
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA encoding H
163 chain V region version r of humanized anti-HM1.24
164 antibody
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(417)
170 <220> FEATURE:
171 <221> NAME/KEY: sig_peptide
172 <222> LOCATION: (1)..(57)
174 <220> FEATURE:
175 <221> NAME/KEY: mat_peptide
176 <222> LOCATION: (58)..(417)
178 <400> SEQUENCE: 3
179 atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt 48
180 Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
181          -15          -10          -5
183 gct cac tcc' cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
184 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
185          -1 1          5          10
187 cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144
188 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
189          15          20          25
191 act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192
192 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
193 30          35          40          45
195 gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240
196 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
197          50          55          60
199 cag aag ttc aag ggc aga gtc acc atg acc gca gac aag tcc acg agc 288
200 Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser
201          65          70          75
203 aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336
204 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val

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205          80          85          90
207 tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384
208 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
209          95          100          105
211 tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418
212 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
213 110          115          120
217 <210> SEQ ID NO: 4
218 <211> LENGTH: 418
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA encoding H
224 chain V region version s of anti-HM1.24 antibody
226 <220> FEATURE:
227 <221> NAME/KEY: CDS
228 <222> LOCATION: (1)..(417)
230 <220> FEATURE:
231 <221> NAME/KEY: sig_peptide
232 <222> LOCATION: (1)..(57)
234 <220> FEATURE:
235 <221> NAME/KEY: mat_peptide
236 <222> LOCATION: (58)..(417)
238 <400> SEQUENCE: 4
239 atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt 48
240 Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
241          -15          -10          -5
243 gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
244 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
245          -1 1          5          10
247 cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144
248 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
249          15          20          25
251 act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192
252 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
253 30          35          40          45
255 gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240
256 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
257          50          55          60
259 cag aag ttc aag ggc aga gtc acc atc acc gca gac aag tcc acg agc 288
260 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
261          65          70          75
263 aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336
264 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
265          80          85          90
267 tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384
268 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
269          95          100          105
271 tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418

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272 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 273 110 115 120

276 <210> SEQ ID NO: 5

277 <211> LENGTH: 180

278 <212> TYPE: PRT

279 <213> ORGANISM: Homo sapiens

281 <220> FEATURE:

282 <223> OTHER INFORMATION: Amino acid sequence of HM1.24 antigen

284 <400> SEQUENCE: 5

285 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

286 1 5 10 15

288 Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu

289 20 25 30

291 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala

292 35 40 45

294 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

295 50 55 60

297 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

298 65 70 75 80

300 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

301 85 90 95

303 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

304 100 105 110

306 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

307 115 120 125

309 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

310 130 135 140

312 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

313 145 150 155 160

315 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser

316 165 170 175

318 Ala Leu Leu Gln

319 180

322 <210> SEQ ID NO: 6

323 <211> LENGTH: 126

324 <212> TYPE: PRT

325 <213> ORGANISM: Artificial Sequence

327 <220> FEATURE:

328 <223> OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence

329 of L chain V region version a of humanized anti-HM1.24

330 antibody

332 <400> SEQUENCE: 6

333 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

334 -15 -10 -5

336 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

337 -1 1 5 10

339 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val

340 15 20 25

342 Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/760,723

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